## Chiara Pontremoli

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3842978/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	OASes and STING: Adaptive Evolution in Concert. Genome Biology and Evolution, 2015, 7, 1016-1032.	2.5	57
2	Genetic susceptibility to infectious diseases: Current status and future perspectives from genome-wide approaches. Infection, Genetics and Evolution, 2018, 66, 286-307.	2.3	48
3	Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. Molecular Biology and Evolution, 2014, 31, 2402-2414.	8.9	28
4	REST, a master regulator of neurogenesis, evolved under strong positive selection in humans and in non human primates. Scientific Reports, 2017, 7, 9530.	3.3	27
5	Antigenic variation of SARS oVâ€⊋ in response to immune pressure. Molecular Ecology, 2021, 30, 3548-3559.	3.9	27
6	Arenavirus genomics: novel insights into viral diversity, origin, and evolution. Current Opinion in Virology, 2019, 34, 18-28.	5.4	26
7	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host–Virus Codivergence. Genome Biology and Evolution, 2018, 10, 863-874.	2.5	22
8	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. Molecular Biology and Evolution, 2020, 37, 1259-1271.	8.9	22
9	Past and ongoing adaptation of human cytomegalovirus to its host. PLoS Pathogens, 2020, 16, e1008476.	4.7	19
10	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. Genome Biology and Evolution, 2015, 7, 2569-2584.	2.5	16
11	Positive Selection Drives Evolution at the Host–Filovirus Interaction Surface. Molecular Biology and Evolution, 2016, 33, 2836-2847.	8.9	16
12	The mammalian complement system as an epitome of host–pathogen genetic conflicts. Molecular Ecology, 2016, 25, 1324-1339.	3.9	15
13	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. Frontiers in Microbiology, 2018, 9, 854.	3.5	15
14	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. BMC Evolutionary Biology, 2017, 17, 43.	3.2	14
15	Possible European Origin of Circulating Varicella Zoster Virus Strains. Journal of Infectious Diseases, 2020, 221, 1286-1294.	4.0	13
16	Positive selection underlies the speciesâ€specific binding of <i>Plasmodium falciparum </i> <scp>RH</scp> 5 to human basigin. Molecular Ecology, 2015, 24, 4711-4722.	3.9	12
17	The CCR5î"32 allele is not a major predisposing factor for severe H1N1pdm09 infection. BMC Research Notes, 2014, 7, 504.	1.4	11
18	Diverse selective regimes shape genetic diversity at <i>ADAR</i> genes and at their coding targets. RNA Biology, 2015, 12, 149-161.	3.1	9

CHIARA PONTREMOLI

#	Article	IF	CITATIONS
19	A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. Microbes and Infection, 2017, 19, 69-74.	1.9	9
20	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. Nucleic Acids Research, 2018, 46, 7153-7168.	14.5	8
21	Kinetochore proteins and microtubuleâ€destabilizing factors are fast evolving in eutherian mammals. Molecular Ecology, 2021, 30, 1505-1515.	3.9	8
22	Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. Molecular Ecology, 2017, 26, 5173-5188.	3.9	7
23	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. Infection, Genetics and Evolution, 2018, 64, 212-218.	2.3	6
24	Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. Molecular Biology and Evolution, 2022, 39, .	8.9	3
25	Multiple Selected Changes May Modulate the Molecular Interaction between Laverania RH5 and Primate Basigin. MBio, 2018, 9, .	4.1	2
26	Variants in the CYP7B1 gene region do not affect natural resistance to HIV-1 infection. Retrovirology, 2015, 12, 80.	2.0	1
27	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. Virus Evolution, 2021, 7, veab040.	4.9	Ο